



## **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/623,854  
Source: OIPF  
Date Processed by STIC: 8/1/2003

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

Raw Sequence Listing Error Summary

**ERROR DETECTED**

**SUGGESTED CORRECTION**

SERIAL NUMBER:

10/623,854

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ✓ Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
                                    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                    This sequence is intentionally skipped  
  
                                    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
                                    <210> sequence id number  
                                    <400> sequence id number  
                                    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                                    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                                    In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>      Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
                                    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

see item 4 on Error summary  
sheet

10/623,854 1

delete  
□y"z-ñ•\□z  
SEQUENCE LISTING

<110> NARA INSTITUTE OF SCIENCE AND TECHNOLOGY

<120> Multiple use of caffeine biosynthetic genes

<130> 19-023

<140>

<141>

<150> JP 2002-213655

<151> 2002-07-23

<160> 9

<170> Microsoft Word

<210> 1

<211> 372

<212> PRT

<213> ←

<300>

<301> Ogawa, M., Herai, Y., Koizumi, N., Kusano, T., and Sano, H.

<302> 7-Methylxanthine Methyltransferase of Coffee Plants. Gene Isolation and Enzymatic Properties.

<303> Journal of Biological Chemistry

<304> 276

<305> 11

<306> 8213-8218

<307> 2001-03-16

<308> BAB39215

<309> 2000-09-11

<400> 1--

Met Glu Leu Gln Glu Val Leu Arg Met Asn Gly Gly Glu Gly

1 5 10

Asp Thr Ser Tyr Ala Lys Asn Ser Ala Tyr Asn Gln Leu Val

15 20 25

Leu Ala Lys Val Lys Pro Val Leu Glu Gln Cys Val Arg Glu

Leu Leu Arg Ala Asn Leu Pro Asn Ile Asn Lys Cys Ile Lys

Val Ala Asp Leu Gly Cys Ala Ser Gly Pro Asn Thr Leu Leu

Thr Val Arg Asp Ile Val Gln Ser Ile Asp Lys Val Gly Gln

Glu Lys Lys Asn Glu Leu Glu Arg Pro Thr Ile Gln Ile Phe

Leu Asn Asp Leu Phe Pro Asn Asp Phe Asn Ser Val Phe Lys

Leu Leu Pro Ser Phe Tyr Arg Lys Leu Glu Lys Glu Asn Gly

Arg Lys Ile Gly Ser Cys Leu Ile Gly Ala Met Pro Gly Ser

These three  
pages show  
samples of  
global errors

This file  
could not be  
processed -  
invalid  
format

Does Not Comply  
Corrected Diskette Needed

insert this MANDATORY numeric identifier  
AND its response

Please  
re-number  
amino  
acids

delete  
14 invalid  
28 numbering  
42  
56 Per 1.822 of  
70 Sequence Rules,  
84 number the  
98 amino acids  
112 under every 5  
126 amino acids.  
140 Do NOT use TAB codes  
between amino acid  
numbers. Use space  
characters.

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Phe Tyr Ser Arg Leu Phe Pro Glu Glu Ser Met His Phe Leu	154
His Ser Cys Tyr Cys Leu Gln Trp Leu Ser Gln Val Pro Ser	168
Gly Leu Val Thr Glu Leu Gly Ile Ser Thr Asn Lys Gly Ser	182
Ile Tyr Ser Ser Lys Ala Ser Arg Leu Pro Val Gln Lys Ala	196
Tyr Leu Asp Gln Phe Thr Lys Asp Phe Thr Thr Phe Leu Arg	210
Ile His Ser Glu Glu Leu Phe Ser His Gly Arg Met Leu Leu	224
Thr Cys Ile Cys Lys Gly Val Glu Leu Asp Ala Arg Asn Ala	238
Ile Asp Leu Leu Glu Met Ala Ile Asn Asp Leu Val Val Glu	252
Gly His Leu Glu Glu Glu Lys Leu Asp Ser Phe Asn Leu Pro	266
Val Tyr Ile Pro Ser Ala Glu Glu Val Lys Cys Ile Val Glu	280
Glu Glu Gly Ser Phe Glu Ile Leu Tyr Leu Glu Thr Phe Lys	294
Val Leu Tyr Asp Ala Gly Phe Ser Ile Asp Asp Glu His Ile	308
Lys Ala Glu Tyr Val Ala Ser Ser Val Arg Ala Val Tyr Glu	322
Pro Ile Leu Ala Ser His Phe Gly Glu Ala Ile Ile Pro Asp	336
Ile Phe His Arg Phe Ala Lys His Ala Ala Lys Val Leu Pro	350
Leu Gly Lys Gly Phe Tyr Asn Asn Leu Ile Ile Ser Leu Ala	364
Lys Lys Pro Glu Lys Ser Asp Val	372

re-number

correctly

<210> 2  
 <211> 1316  
 <212> DNA  
 <213> Coffea arabica

<220>  
 <221> CDS  
 <222> (45)□c(1163)

<300>  
 <308> AB048793  
 <309> 2000-09-11

<400> 2	
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ctccaagaag tcttgccgat gaatggaggc gaaggcgata caagctacgc	100
caagaattca gcctacaatc aactggttct cgccaagggtg aaacctgtcc	150
ttgaacaatg cgtacgggaa ttgttgccggg ccaacttgcc caacatcaac	200

delete this (please delete ALL instances of this format  
 marker  
 throughout  
 sequence listing)

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<210> 4  
 <211> *mandatory response needed*  
 <212> PRT  
 <213> Coffea arabica

<400> 4	
Met Glu Leu Gln Glu Val Leu His Met Asn Glu Gly Glu Gly	14
Asp Thr Ser Tyr Ala Lys Asn Ala Ser Tyr Asn Leu Ala Leu	28
Ala Lys Val Lys Pro Phe Leu Glu Gln Cys Ile Arg Glu Leu	42
Leu Arg Ala Asn Leu Pro Asn Ile Asn Lys Cys Ile Lys Val	56
Ala Asp Leu Gly Cys Ala Ser Gly Pro Asn Thr Leu Leu Thr	70
Val Arg Asp Ile Val Gln Ser Ile Asp Lys Val Gly Gln Glu	84
Glu Lys Asn Glu Leu Glu Arg Pro Thr Ile Gln Ile Phe Leu	98
Asn Asp Leu Phe Gln Asn Asp Phe Asn Ser Val Phe Lys Leu	112
Leu Pro Ser Phe Tyr Arg Lys Leu Glu Lys Glu Asn Gly Arg	126
Lys Ile Gly Ser Cys Leu Ile Ser Ala Met Pro Gly Ser Phe	140
Tyr Gly Arg Leu Phe Pro Glu Glu Ser Met His Phe Leu His	154
Ser Cys Tyr Ser Val His Trp Leu Ser Gln Val Pro Ser Gly	168
Leu Val Ile Glu Leu Gly Ile Gly Ala Asn Lys Gly Ser Ile	182
Tyr Ser Ser Lys Ala Ser Arg Pro Pro Val Gln Lys Ala Tyr	196
Leu Asp Gln Phe Thr Lys Asp Phe Thr Thr Phe Leu Arg Ile	210
His Ser Lys Glu Leu Phe Ser Arg Gly Arg Met Leu Leu Thr	224
Cys Ile Cys Lys Val Asp Glu Tyr Asp Glu Pro Asn Pro Leu	238
Asp Leu Leu Asp Met Ala Ile Asn Asp Leu Ile Val Glu Gly	252
His Leu Glu Glu Glu Lys Leu Ala Ser Phe Asn Leu Pro Phe	266
Phe Thr Pro Ser Ala Glu Glu Val Lys Cys Ile Val Glu Glu	280
Glu Gly Ser Phe Glu Ile Leu Tyr Leu Glu Thr Phe Lys Ala	294
His Tyr Asp Ala Gly Phe Ser Ile Asp Asp Asp Tyr Pro Val	308
Arg Ser His Phe Gln Val Tyr Gly Asp Glu His Ile Lys Ala	322
Glu Tyr Val Ala Ser Leu Ile Arg Ser Val Tyr Glu Pro Ile	336
Leu Ala Ser His Phe Gly Glu Ala Ile Met Pro Asp Leu Phe	350
His Arg Leu Ala Lys His Ala Ala Lys Val Leu His Leu Gly	364

*delete  
re-number  
correctly*

*Please ensure that all nucleotides  
and amino acids are valid.*

The types of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.